

&lt;!--StartFragment--&gt;RESULT 1

JC8067

mitochondrial C1-tetrahydrofolate synthetase - human

C;Species: Homo sapiens (man)

C;Date: 09-May-2004 #sequence\_revision 09-May-2004 #text\_change 05-Oct-2004

C;Accession: JC8067

R;Sugiura, T., Nagano, Y., Inoue, T., and Hirotani, K.

Biochem. Biophys. Res. Commun. 315, 204-211, 2004

A;Title: A novel mitochondrial C1-tetrahydrofolate synthetase is upregulated in human colon adenocarcinoma.

A;Reference number: JC8067; PMID: 15013446

A;Accession: JC8067

A;Molecule type: mRNA

A;Residues: 1-978 &lt;SUG&gt;

A;Cross-references: GB:AL117452

C;Comment: This enzyme, which is a trifunctional enzyme, participates in the progression of colorectal cancer by conferring growth advantage and is a new molecular target for colon cancer therapy. It is important in catalysis of reactions in the one-carbon metabolic pathway and is capable of accelerating cell proliferation.

C;Genetics:

A;Gene: DKFZp586G1517

A;Map position: 6q25.1

C;Superfamily: C1-tetrahydrofolate synthase

C;Keywords: C1-tetrahydrofolate synthetase; colon cancer; one-carbon unit pathway; trifunctional enzyme

Query Match 100.0%; Score 4998; DB 2; Length 978;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-289;  
 Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGTRLPLVLRQLRRPPQPPGPPRRLRVPCRASSGGGGGGGGGREGLLGQRRPQDGQARSS	60
Db	1	MGTRLPLVLRQLRRPPQPPGPPRRLRVPCRASSGGGGGGGGGREGLLGQRRPQDGQARSS	60
Qy	61	CSPGGRTPAARDSIVREVIQNSKEVLSLLQEKNPAFKPVLAI IQAGDDNLMQEINQNLA E	120
Db	61	CSPGGRTPAARDSIVREVIQNSKEVLSLLQEKNPAFKPVLAI IQAGDDNLMQEINQNLA E	120
Qy	121	EAGLNITHICLPPDSSEAEIIDEILKINEDTRVHGLALQISENLF SNKVLNALKPEKDVD	180
Db	121	EAGLNITHICLPPDSSEAEIIDEILKINEDTRVHGLALQISENLF SNKVLNALKPEKDVD	180
Qy	181	GVT DINLGKLV RGDAHECFVSPVAKAVIELLEKSGVNLDGKKILVVG AHGSLEAALQCLF	240
Db	181	GVT DINLGKLV RGDAHECFVSPVAKAVIELLEKSGVNLDGKKILVVG AHGSLEAALQCLF	240
Qy	241	QRKGSMTMSIQWKTRQLQSKLHEADIVVLGSPKP EEIPLTWIQPGTTVLNCSHDFLSGKV	300
Db	241	QRKGSMTMSIQWKTRQLQSKLHEADIVVLGSPKP EEIPLTWIQPGTTVLNCSHDFLSGKV	300
Qy	301	GCGSPRIHFGGLIEEDDVILLAAALRIQNMVSSGRRWLREQQHRRWRLHCLKLQPLSPVP	360
Db	301	GCGSPRIHFGGLIEEDDVILLAAALRIQNMVSSGRRWLREQQHRRWRLHCLKLQPLSPVP	360
Qy	361	SDIEISRGQTPKAVDVLAKEIGLLADEIEIYGKSKAKVRLSVLERLKDQADGKYVLVAGI	420
Db	361	SDIEISRGQTPKAVDVLAKEIGLLADEIEIYGKSKAKVRLSVLERLKDQADGKYVLVAGI	420

Qy	421	TPTPLGEGKSTVTIGLVQALTAHLNVNSFACLRQPSQGPTFGVKGGAAGGGYAQVIPMEE	480
Db	421	TPTPLGEGKSTVTIGLVQALTAHLNVNSFACLRQPSQGPTFGVKGGAAGGGYAQVIPMEE	480
Qy	481	FNLHLTGDIHAITAANNLLAAAIDTRILHENTQTDKALYNRLVPLVNGVREFSEIQLARL	540
Db	481	FNLHLTGDIHAITAANNLLAAAIDTRILHENTQTDKALYNRLVPLVNGVREFSEIQLARL	540
Qy	541	KKLGINKTDPSTLTETEEVSKFARLDIDPSTITWQRVLDTNDRFLRKITIGQGNTTEKGHYR	600
Db	541	KKLGINKTDPSTLTETEEVSKFARLDIDPSTITWQRVLDTNDRFLRKITIGQGNTTEKGHYR	600
Qy	601	QAQFDIAVASEIMAVLALTDLSADMKARLGRMVVASDKSGQPVTADDLGVTGALTVMKD	660
Db	601	QAQFDIAVASEIMAVLALTDLSADMKARLGRMVVASDKSGQPVTADDLGVTGALTVMKD	660
Qy	661	AIKPNLMQTLEGTPVFVHAGPFANIAHGNSSVLADKIALKLVGEEGFVVTEAGFGADIGM	720
Db	661	AIKPNLMQTLEGTPVFVHAGPFANIAHGNSSVLADKIALKLVGEEGFVVTEAGFGADIGM	720
Qy	721	EKFFNIKCRASGLVPNVVVLVATVRALKMHGGGPSVTAGVPLKKEYTEENIQLVADGCCN	780
Db	721	EKFFNIKCRASGLVPNVVVLVATVRALKMHGGGPSVTAGVPLKKEYTEENIQLVADGCCN	780
Qy	781	LQKQIQITQLFGVPVVVALNVFKTDTRAIEDLVCELAKRAGAFDAVPCYHWSVGKGKGSVD	840
Db	781	LQKQIQITQLFGVPVVVALNVFKTDTRAIEDLVCELAKRAGAFDAVPCYHWSVGKGKGSVD	840
Qy	841	LARAVREAASKRSRFQFLYDVQVPIVDKIRTIAQAVYGAKDIELSPEAQAKIDRYTQQGF	900
Db	841	LARAVREAASKRSRFQFLYDVQVPIVDKIRTIAQAVYGAKDIELSPEAQAKIDRYTQQGF	900
Qy	901	GNLPICMAKTHLSLSHQPKKGVPDRDFILPISDVRASIGAGFIYPLVGTMTMPGLPTRP	960
Db	901	GNLPICMAKTHLSLSHQPKKGVPDRDFILPISDVRASIGAGFIYPLVGTMTMPGLPTRP	960
Qy	961	CFYDIDLDTETEQVKGLF	978
Db	961	CFYDIDLDTETEQVKGLF	978

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